Claims:

1.: Method for analysing DNA of a sweet potato, characterised in by the following steps:

- providing DNA of a sweet potato,
- physically breaking said DNA into DNA pieces,
- introducing known sequences at at least one of the two ends of each DNA piece,
- providing at least two primers, a first primer according to the formula

$$(N_x)_nAGTCCTAACAN_1N_2N_3 \quad (I)$$

wherein N_x is selected from A, C, G and T; n is 0 to 20; N_1 is G, T, A or not present; N_2 is A, C, G or not present; N_3 is A, C, G or not present; or a complementary sequence thereto; and a second primer being able to anneal to the introduced sequence,

- amplifying DNA of the DNA pieces with said primers and
- analysing said amplified DNA.

2.: Method according to claim 1, characterised in that said physically breaking is performed by restriction endonuclease digestion, preferably by a digestion with a 6 bp cutting enzyme, especially a rare cutting enzyme.

3.: Method according to claim 1 or 2, characterised in that $(N_x)_4$ residues are selected from the sequence AGACTAAG.

4.: Method according to any one of claims 1 to 3, characterised in that said first primer comprising a sequence selected from AGACTAAGAGTCCTAACA, AGACTAAGAGTCCTAACAG, AGACTAAGAGTCCTAACAT, AGACTAAGAGTCCTAACAA, AGACTAAGAGTCCTAACAGC, AGACTAAGAGTCCTAACAGA, AGACTAAGAGTCCTAACAGG, AGACTAAGAGTCCTAACATA, AGACTAAGAGTCCTAACATG, AGACTAAGAGTCCTAACATC, AGACTAAGAGTCCTAACAAA, AGACTAAGAGTCCTAACAAG, AGACTAAGAGTCCTAACAAC, or fragments thereof, said fragments optionally comprising at least 10 bp of the 3' part of said sequences.

5.: Method according to any one of claims 1 to 4, characterised in that said introducing known sequences at at least one of the two ends of each DNA piece

comprises cutting the DNA with a restriction enzyme and linking an adapter to the end, said adapter comprising a known sequence.

6.: Method according to any one of claims 1 to 5, characterised in that said analysing comprises separating the amplified nucleic acid molecules by size.

7.: Method for defining the phylogenetic and geographical relationship of two or more sweet potatoes having different genotypes, comprising performing a method according to any one of claims 1 to 6 on each sweet potato and comparing the results.

8.: Method according to claim 7, characterised in that said comparing step comprises analysing a size separation of amplified nucleic acids.

9.: Method according to claim 7 or 8, characterised in that said comparing is performed by a computer calculating the phylogenetic distance from a size separation of amplified nucleic acids.

10.: Kit for performing a method according to any one of claims 1 to 9, characterised in that it comprises at least two primers as defined in any one of claims 1 to 9 and a nucleic acid polymerase for amplifying nucleic acids defined by said at least two primers.

11.: Nucleic acid molecule comprising
(a) a sequence of the formula

$$(N_x)_oAGTCCTAACA(N_x)_m \qquad (II)$$

wherein N_x is selected from A, C, G and T; m and o are independently from each other 0 to 1000, or
(b) sequences differing not more than 1 b/bp per 20 b/bp from the sequence of the formula (II) or,
(c) sequences hybridizing under stringent conditions to the sequence of the formula (II) or
(d) complementary sequences to (a), (b) or (c).

12.: Nucleic acid molecule according to claim 11, characterised in that it comprises Seq. ID. No.1.